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Molecular phylogenetics of six marine microalgae strains from Greek transient waters

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Scope of the study

- AthU-Al (Athens University Algae) culture collection of the NKUA preserves strains isolated from various Greek coastal lagoons
- Strains studied: AthU-Al Mes5, AthU-Al Mes17, AthU-Al Dun30, AthU-Al Dun31, AthU-Al Dun32 and AthU-Al T_3_1
- Molecular markers: nuclear ITS region and 18S rDNA, plastid *rbcl* and *tufA*
- *TufA* and *rbcL* markers were selected to generate a phylogenetic tree based on their concatenated sequences

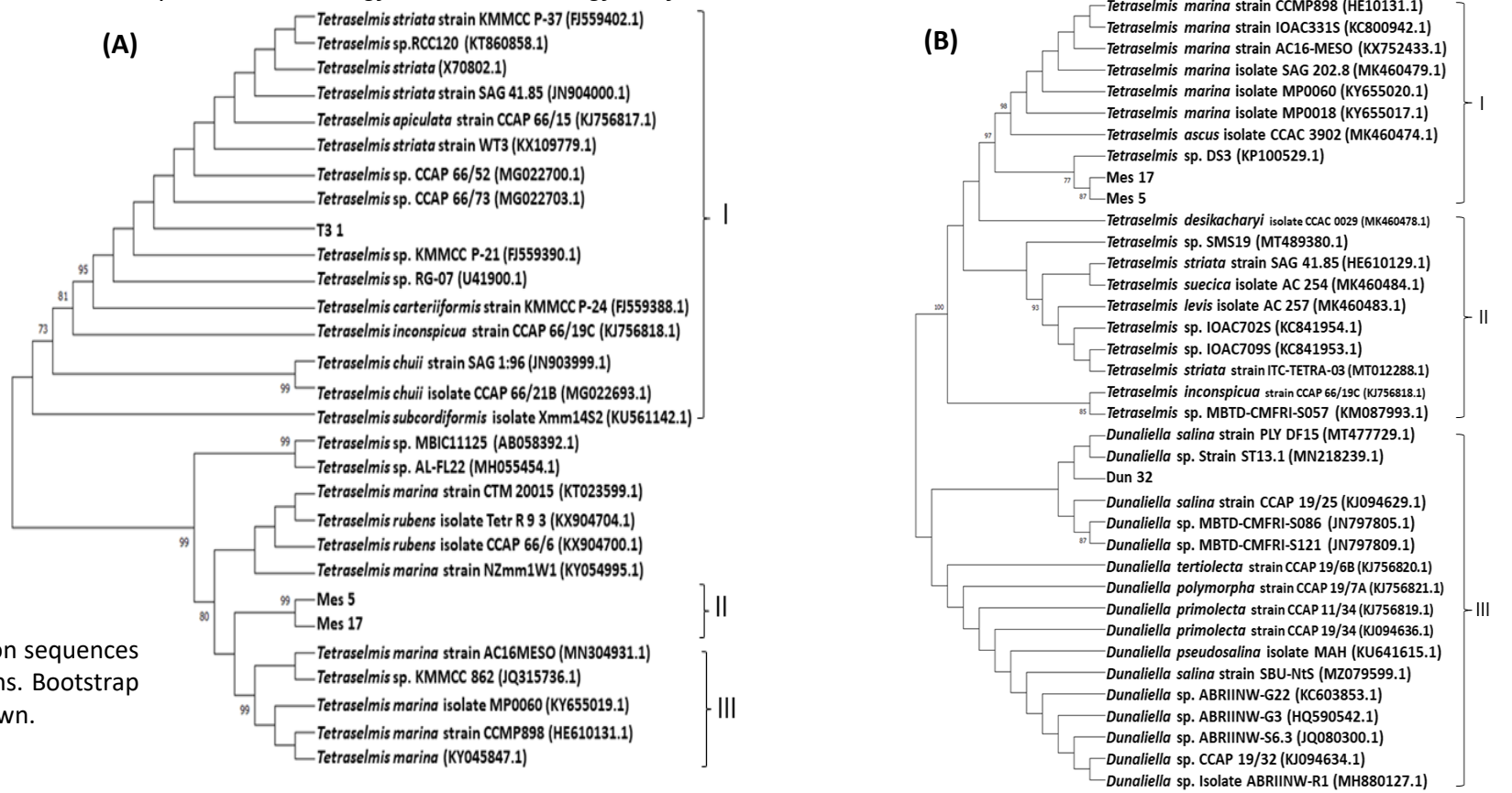
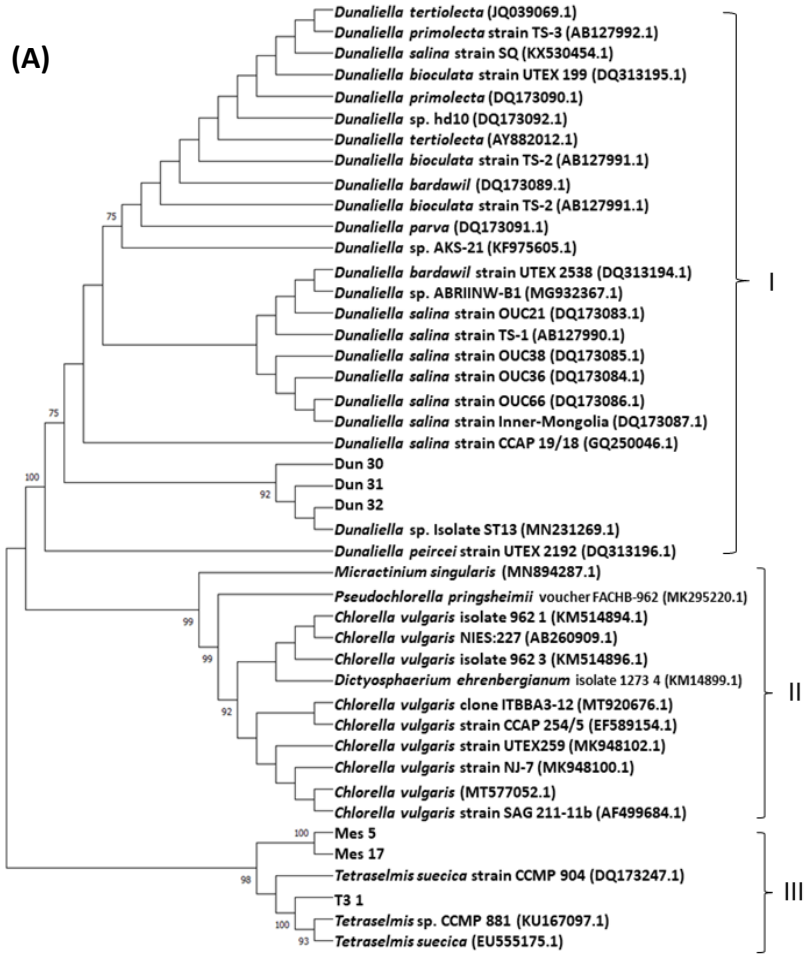


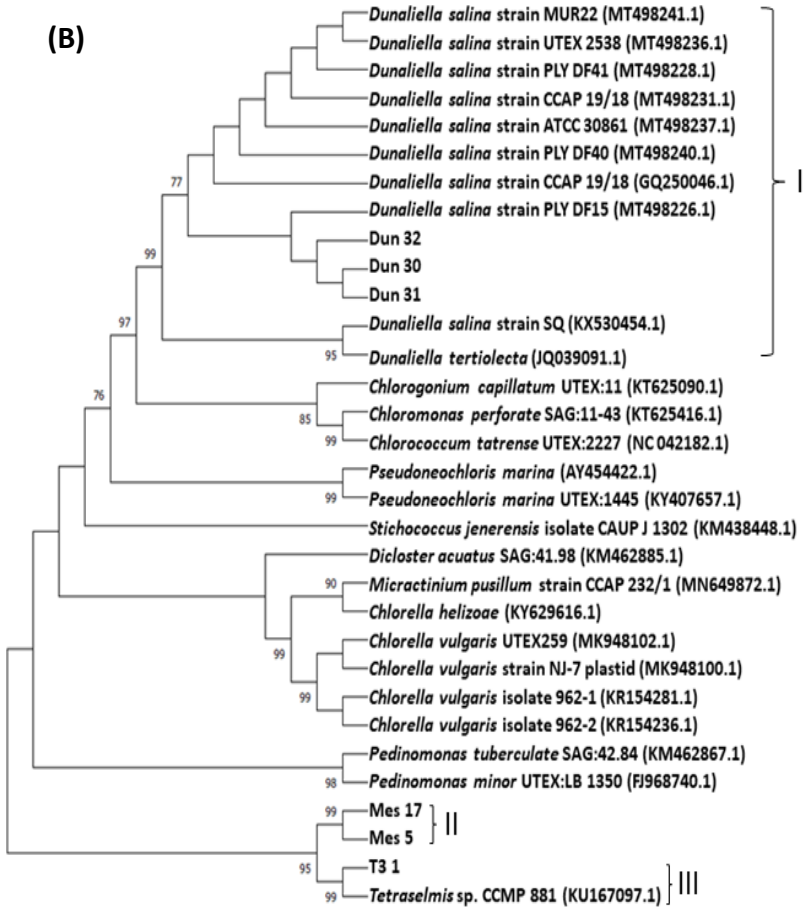
Fig 1. Maximum likelihood trees of **(A)** 18S rDNA and **(B)** *ITS* region sequences showing the phylogenetic relationship of studied microalgal strains. Bootstrap confident levels (based on 1000 replicates) below 70% are not shown.

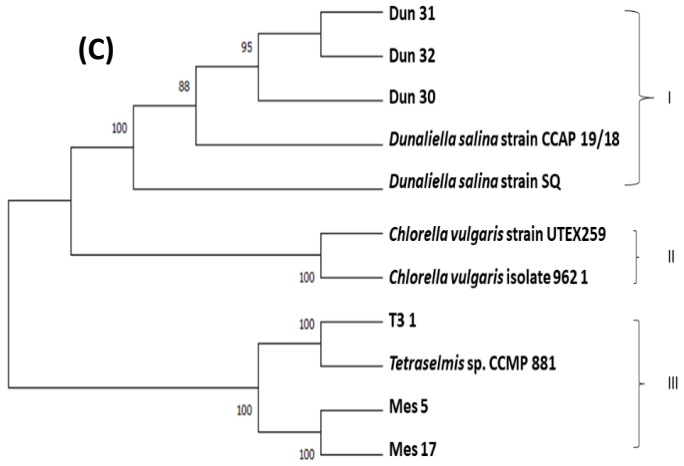
- **Clade I**: T3_1 shares 98.77% to 99.78% similarity with the reference strains comprised in the clade.
- **Clade II**: Mes_5 and Mes_17 share 99.78% similarity between them and form a separate lineage, in the vicinity of their closest relative *T. marina* NZmm1W1.

- **Clade I**: Mes_5 and Mes_17 strains are 100% identical and share 92.99% similarity with *T. desikacharyi.*
- **Clade III**: Dun_32 share 99.42% similarity with its closest relative *D. salina* strain PLY DF15.

Fig 2. Maximum likelihood trees of **(A)** *rbcl* and **(B)** *TufA* genes sequences showing the phylogenetic relationship of studied microalgal strains. **(C)** Concatenated tree of the genes *rbcl* and *TufA*. Bootstrap confident levels (based on 1000 replicates) below 70% are not shown.







- **Clade I**: Dun_30, Dun_31 and Dun_32 are 100% identical, and cluster together with *Dunaliella* sp. isolate ST13.
- **Clade III**: T3_1 shares 98.78% similarity with its closest relative *Tetraselmis* sp. CCMP 881. Mes_5 and Mes_17 are 100% identical and cluster together within the clade, in a separate lineage.

- **Clade I**: Dun_30, Dun_31 and Dun_32 share 100% identity with several *D. salina* strains included in the group.
- **Clade II**: Identical Mes_5 and Mes_17 strains are placed in a branch, in the vicinity of *Tetraselmis* sp.
- **Clade III**: T3_1 shares 97.87% similarity with its closest reference strain *Tetraselmis* sp. CCMP 881.

- Concatenation of the *rbcl* and *Tuf A* gene sequences, produced a more robust phylogeny of the selected strains, which was consistent with the topologies obtained from the individual genes.
- **Clade I**: Dun_30, Dun_31 and Dun_32 strains share 99.52% similarity with their closest related reference strain *D. salina* (CCAP 19/18).
- **Clade III**: T3_1 shares 98.80% similarity with *Tetraselmis* sp. CCMP 881, whereas Mes_5 and Mes_17 both share 92.99% similarity with *Tetraselmis* sp. CCMP 881.

Conclusions

- The studied *Dunaliella* strains are placed within the species *D. salina,* finding in line with previously obtained biochemical data.
- According to the described gene phylogenies, strains Mes_5 and Mes_17 are 100% identical.
- Phylogenetic analysis revealed that, within the genus *Tetraselmis,* exist complex and unresolved relationships indicating the need for a more in-depth investigation of unidentified strains with a multi-gene approach.